OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 16:58:04 ; Search time 661.571 seconds
(without alignments)
122.492 Million cell updates/sec

Title: US-09-856-070-26
Perfect score: 28
Sequence: 1 QDYEF 5

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 3230813?

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL-frame-p2n model -NPV-xif
-Q-/cgr3_1/US7/c.spool/US0085070/runat_1101_2003_1554_4_h_4/ppt_query fasta_1 1552
-DB-EST -QFMT-fastap SUFFIX-rst -MINMATCH 0.1 -LENPCT-0 -LENPEXT=0
-(UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TPANS-human40 cdi -LIST-45
-DOFALIGN-200 -THE_SCORE=pct -THR_MAX=100 -THR_MIN=0 -MAXLEN-2000000000
-OUTFMT-ptg -NORM-txt -HEAPSIZE-500 -MINLEN=0 -MAXLEN=2000000000
-USER-US0985070_405N_1_1_4322-runat_1101_2003_1554_4_h_4 -NPEV- TIMEOUT-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LCN=LOG -NEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP 6 -FGAPEXT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database:
RST:
1: em_estba: *
2: em_esthum: *
3: em_estin *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_esthun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_lun: *
23: em_gss_man: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_FT?: *
27: em_gss_rod: *

SUMMARIES

Result No.	Pred. No.	Score	% Query Match	Length	DB	ID	Description
1	0	28	100.0	129	12	BF359041	BF359041 RC6-ET004
2		28	100.0	130	12	BC186486	BC186486 RST5661 A
3		28	100.0	130	12	BC193087	BC193087 RST1319
4		28	100.0	139	12	BG219430	BG219430 RST4988
5	0	28	100.0	136	17	BH719297	BH719297 B0MGZ62TR
6	0	28	100.0	137	12	BC216901	BC216901 RST36602
7	0	28	100.0	139	12	BC192394	BC192394 RST11508
8	0	28	100.0	139	12	BC193988	BC193988 RST13130
9	0	28	100.0	142	9	AI130110	AI130110 SWvvL4CAN
10		28	100.0	148	10	BE170685	BE170685 QV4-HT053
11		28	100.0	154	12	BG192932	BG192932 RST12057
12		28	100.0	157	14	HM844888	HM844888 K-EST0123
13		28	100.0	159	10	AW867176	AW867176 MH1-SN003
14		28	100.0	164	13	B1013708	B1013708 PM3-ET020
15	0	28	100.0	167	17	A2227319	A2227319 RFC2 23-4
16		28	100.0	174	12	BG181469	BG181469 RST317 At
17		28	100.0	178	12	BE701599	BE701599 QV0-NN018
18	0	28	100.0	180	10	AW943769	AW943769 PC4-NN002
19		28	100.0	180	17	A2120611	A2120611 RFC1-23-4
20	0	28	100.0	189	9	AA709283	AA709283 ai2ljo2.s
21		28	100.0	192	10	AW86.2068	AW86.2068 RC3-CT034
22		28	100.0	200	9	AA04133	AA04133 zi47h03.r
23		28	100.0	202	9	AA834433	AA834433 o168e06.r
24		28	100.0	204	14	F28680	F28680 MUS89A08 mo
25	0	28	100.0	205	13	BJ170217	BJ170217 BJ170.47
26		28	100.0	209	9	A155.4155	A155.4155 i.St0589
27		28	100.0	211	10	AW044476	AW044476 sd-zytc5.y
28	0	28	100.0	211	13	BI032528	BI032528 FM3-NN117
29		28	100.0	214	9	AA512426	AA512426 th01a07.s
30	0	28	100.0	214	12	BE811484	BE811484 MR3-AN002
31		28	100.0	214	10	BE845878	BE845878 PC5-CN028
32	0	28	100.0	214	13	BI054473	BI054473 PC5-CN028
33		28	100.0	215	12	BE811585	BE811585 ME3 AN002
34		28	100.0	215	14	BQ367833	BQ367833 RC5-GN028
35		28	100.0	219	14	H42989	H42989 7611-02.s1
36		28	100.0	225	10	BF041144	BF041144 hk47-11.y
37		28	100.0	225	12	BF043361	BF043361 hk27-02.y
38	0	28	100.0	225	14	F31733	F31733 HSP23118 H
39		28	100.0	230	14	H41269	H41269 yn89107.s1
40	0	28	100.0	232	12	BF942201	BF942201 QV2-NN004
41	0	28	100.0	234	12	BG754562	BG754562 F0271C344
42	0	28	100.0	234	13	BM319839	BM319839 k179a11.7
43		28	100.0	241	9	AA293911	AA293911 SWOv3MCA1
44		28	100.0	246	9	HH15.2615	HH15.2615 HH4t2615
45	0	28	100.0	251	9	AI872684	AI872684 wn08e08.x

ALIGNMENTS

RESULT 1
BF359041/c
LOCUS BF359041 129 bp mRNA linear EST 22-NOV-2000
DEFINITION RC6-ET004-230900-011-010 ET004 Homo sapiens cDNA. mRNA sequence.
ACCESSION BF359041
VERSION BF359041.1 GI:11318113
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE   Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
          ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
          Simpson,A.J.
          Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U S A 97 (7), 3491-3496 (2000)
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?tbl RG6&t2-HCF-F1004F
          28000-013-R10&t2000-06-28&t4-1)
          Seq primer: puc 18 forward
          High quality sequence start: 14
          High quality sequence stop: 129.
FEATURES   Location/Qualifiers
     source   1..129
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib=" BT0046"
                     /dev_stage="Adult"
                     /note="organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT   27 a   37 c   29 g   36 t
ORIGIN

Alignment Scores:
Pred. No.:   1e+03   Length: 129
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 12   Gaps: 0

US-09-856-070-26 (1-5) x BF359041 (1-129)

Qy   1 GlnAspTyrGluGlu 5
         |||||||||||||||
Db   41 CAGGACTACGAAGAA 27

RESULT 2
BG186686
LOCUS   BG186686   130 bp   mRNA   linear   EST 21-APR-2001
DEFINITION RST5661 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG186686
VERSION   BG186686.1 GI:13708373
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 130)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J
            ., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE   Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151

COMMENT   Contact: Scott J. Cain
          Athersys, Inc.
          3201 Carnegie Ave, Cleveland, OH 44115, USA
          Tel: 216 431 9900
          Fax: 216 361 9596
          Email: scain@athersys.com
          High quality sequence stop: 130.
FEATURES   Location/Qualifiers
     source   1..130
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT   49 a   21 c   27 g   33 t
ORIGIN

Alignment Scores:
Pred No.:   1.01e+03   Length: 130
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 12   Gaps: 0

US-09-856-070-26 (1-5) x BG186686 (1-130)

Qy   1 GlnAspTyrGluGlu 5
         |||||||||||||||
Db   66 CAAGATTACGAAGAG 80

RESULT 3
BG193987
LOCUS   BG193987   130 bp   mRNA   linear   EST 21-APR-2001
DEFINITION RST13129 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG193987
VERSION   BG193987.1 GI:13715674
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 130)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J
            ., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,J., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE   Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151

COMMENT   Contact: Scott J. Cain
          Athersys, Inc.
          3201 Carnegie Ave, Cleveland, OH 44115, USA
          Tel: 216 431 9900
          Fax: 216 361 9596
          Email: scain@athersys.com
          High quality sequence stop: 130.
FEATURES   Location/Qualifiers
     source   1..130
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT   51 a   21 c   27 g   31 t
ORIGIN

Alignment Scores:
Pred. No.:   1.01e+03   Length: 130
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 12   Gaps: 0

US-09-856-070-26 (1-5) x BG219987 (1-130)

Qy   1 GlnAspTyrGluGlu 5
         ||||||||||||||
Db   66 CAAGATTACGAAGAG 80

RESULT 4
LOCUS   BG219430
DEFINITION   RST39188 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG219430
VERSION   BG219430.1 GI:13745451
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 130)
AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P., Perry,P.,
             Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
             ,Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
             ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Io,K., Offenbacher
             ,J., Danzig,J. and Ducar,M.
TITLE   Creation of genome-wide protein expression libraries using random
             activation of gene expression
JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE   21227151
COMMENT   Contact: Scott J. Cain
             Athersys, Inc.
             3201 Carnegie Ave, Cleveland, OH 44115, USA
             Tel: 216 431 9900
             Fax: 216 361 9596
             Email: scain@athersys.com
             High quality sequence stops: 104.
FEATURES   Location/Qualifiers
source   1..130
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_lib="Athersys RAGE Library"
             /cell_line="HT1080"
             /note="See 'Creation of Genome-Wide Protein Expression
             libraries using Random Activation of Gene Expression',
             Nature Biotechnology, in press. Note that even though the
             cell type indicated is HT1080, since a random activation
             method was used, these sequence tags are not necessarily
             expressed in HT1080 under normal circumstances."

BASE COUNT   51 a   22 c   27 g   30 t
ORIGIN

Alignment Scores:
Pred. No.:   1.01e+03   Length: 130
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 12   Gaps: 0

US-09-856-070-26 (1-5) x BG219430 (1-130)

Qy   1 GlnAspTyrGluGlu 5
         ||||||||||||||
Db   66 CAAGATTACGAAGAG 80

RESULT 5
BH719297/C
LOCUS   BH719297   136 bp   DNA   linear   GSS 20 FEB 2002
DEFINITION   BOMGZ62TF BO_2_2_KB Brassica oleracea genomic clone BOMGZ62, DNA
             sequence.
ACCESSION   BH719297
VERSION   BH719297.1 GI:18818901
KEYWORDS   GSS.
SOURCE   Brassica oleracea.
ORGANISM   Brassica oleracea
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 136)
AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE   Whole genome shotgun sequencing of Brassica oleracea
JOURNAL   Unpublished (2001)
COMMENT   Other GSSs: BOMGZ62TF
             Contact: Chris Town
             TIGR
             9712 Medical Center Drive, Rockville, MD 20850, USA.
             Tel: 301-838-3523
             Fax: 301-838-0208
             Email: cdtown@tigr.org
             DNA is from a doubled haploid provided by Tom Osborn.
             Seq primer: TR
             Class: sheared ends.
FEATURES   Location/Qualifiers
source   1..136
             /organism="Brassica oleracea"
             /strain="TO1000DH3"
             /db_xref="taxon:3712"
             /clone="BOMGZ62"
             /clone_lib="HO_2_3_KB"
             /note="vector: pHOS1; site1: BstXI; 2-3 kb sheared
             genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT   24 a   38 c   21 g   53 t
ORIGIN

Alignment Scores:
Pred. No.:   1.08e+03   Length: 136
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 17   Gaps: 0

US-09-856-070-26 (1-5) x BH719297 (1-136)

Qy   1 GlnAspTyrGluGlu 5
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Db   42 CAAGATTACGAGGAA 28

RESULT 6
BG216901/C
LOCUS   BG216901   137 bp   mRNA   linear   EST 21 APR 2001
DEFINITION   RST36632 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG216901
VERSION   BG216901.1 GI:13742922
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 137)
AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P., Perry,P.,
             Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
             ,Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
             ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Io,K., Offenbacher

TITLE   ,J., Danzig,J. and Ducar,M.
           Creation of genome-wide protein expression libraries using random
           activation of gene expression
JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE   21227151
COMMENT   Contact: Scott J. Cain
           Athersys, Inc.
           3201 Carnegie Ave, Cleveland, OH 44115, USA
           Tel: 216 431 9900
           Fax: 216 361 9596
           Email: scain@athersys.com
           High quality sequence stop: 137.
FEATURES   Location/Qualifiers
     source   1..137
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="Athersys RAGE Library"
                /cell_line="HT1080"
                /note="See 'Creation of Genome-wide Protein Expression
                Libraries using Random Activation of Gene Expression',
                Nature Biotechnology, in press. Note that even though the
                cell type indicated is HT1080, since a random activation
                method was used, these sequence tags are not necessarily
                expressed in HT1080 under normal circumstances."
BASE COUNT   33 a   31 c   23 g   50 t
ORIGIN

Alignment Scores:
Pred. No.:   1.09e+03   Length: 137
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Host Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 12   Gaps: 0

US-09-856-070-26 (1-5) x HC216901 (1-137)

Qy   1 GlnAspTyrGluGlu 5
        |||||||||||||||
Db   72 CAAGATTACGAAGAG 58

RESULT 7
HC216901
LOCUS   HC216901   137 bp   mRNA   linear   EST 21-APR-2001
DEFINITION RST11508 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   HC216901
VERSION   HC216901.1 GI:13714081
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 137)
AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
TITLE   Creation of genome-wide protein expression libraries using random
            activation of gene expression
JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE   21227151
COMMENT   Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 139.
FEATURES   Location/Qualifiers
     source   1..139
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone_lib="Athersys RAGE Library"
                 /cell_line="HT1080"
                 /note="See 'Creation of Genome-wide Protein Expression
                 Libraries using Random Activation of Gene Expression',
                 Nature Biotechnology, in press. Note that even though the
                 cell type indicated is HT1080, since a random activation
                 method was used, these sequence tags are not necessarily
                 expressed in HT1080 under normal circumstances."
BASE COUNT   35 a   30 c   23 g   50 t
ORIGIN

Alignment Scores:
Pred. No.:   1.11e+03   Length: 139
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 12   Gaps: 0

US-09-856-070-26 (1-5) x BG192394 (1-139)

Qy   1 GlnAspTyrGluGlu 5
        |||||||||||||||
Db   74 CAAGATTACGAAGAG 60

RESULT 8
BG193988/c
LOCUS   BG193988   139 bp   mRNA   linear   EST 21-APR-2001
DEFINITION RST11116 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG193988
VERSION   BG193988.1 GI:13715675
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 139)
AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
TITLE   Creation of genome-wide protein expression libraries using random
            activation of gene expression
JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE   21227151
COMMENT   Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 139.
FEATURES   Location/Qualifiers
     source   1..139
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone_lib="Athersys RAGE Library"
                 /cell_line="HT1080"
                 /note="See 'Creation of Genome-wide Protein Expression
                 Libraries using Random Activation of Gene Expression',
                 Nature Biotechnology, in press. Note that even though the
                 cell type indicated is HT1080, since a random activation
                 method was used, these sequence tags are not necessarily
                 expressed in HT1080 under normal circumstances."
BASE COUNT   32 a   31 c   23 g   51 t
ORIGIN

Alignment Scores:
Pred. No.:   1.11e+03   Length: 139
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Host Local Similarity: 100.00%   Mismatches: 0

```
Query Match:          100.00%       Indels:          0
DB:                   12            Gaps:            0

US-09-856-070-26 (1-5) x HG193988 (1-139)

Qy    1 GlnAspTyrGluGlu 5
        |||||||||||||||
Db   74 CAAGATTACGAAGAG 60

RESULT 9
AI130110
LOCUS       AI130110           142 bp    mRNA    linear    EST 26-MAR-1999
DEFINITION  SWOvL3CAN40D04 Onchocerca volvulus infective larva cDNA
            (SAW94WL-OvL3) Onchocerca volvulus cDNA clone onchl856 5' similar
            to WP:T22I5.5 CE04934 TROPONIN T-LIKE PROTEIN ;contains element L1
            L1 repetitive element ;, mRNA sequence.
ACCESSION   AI130110
VERSION     AI130110.1  GI:3600128
KEYWORDS    EST.
SOURCE      Onchocerca volvulus.
ORGANISM    Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 142)
AUTHORS     Williams,S.A., Lizotte-Waniewski,M., Laney,S., Wenhong,L., Hillier
            ,L., Allen,M., Bowles,L., Geisel,S., Jost,S., Kucaba,T., Martin,J.,
            Steptoe,M., Theising,H., White,S., Wylie,T., Chatpell,J., Person,H
            , Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
            Schurk, Pitter,F, Kohn,S., Underwood,K. and Marra,M.
TITLE       Molecular Parasitology OvL3
JOURNAL     Unpublished (1998)
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            The library was constructed by Wenhong Lu. The library is available
            from Dr. S.A. Williams, email genome@smith.edu when requesting this
            clone from Dr. Williams, please reference the Williams lab clone id
            - SWOvL3CAN40D04
            Trace considered overall poor quality
            Putative full length read
            The vector to vector length is 316
            Possible reversed clone: similarity on wrong strand
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..142
                     /organism="Onchocerca volvulus"
                     /strain="Sierra Leone"
                     /db_xref="taxon:6282"
                     /clone="onchl856"
                     /clone_lib="Onchocerca volvulus infective larva cDNA
                     (SAW94WL-OvL3)"
                     /lab_host="XL1-Blue MRF'"
                     /note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2
                     Xho I: Cutaneous filarial nematode parasite of humans.
                     mRNA was prepared from third stage infective larvae of
                     Onchocerca volvulus isolated from mosquitoes 10 days after
                     infection and converted to double stranded cDNA using
                     reverse transcriptase and oligo(di) followed by RNase H
                     and DNApol 1. The library had 1.8 x 10E5 independent
                     recombinants and average insert size was 900 base pairs.
                     The library was constructed by Wenhong Lu. The library is
                     available from Dr. S.A. Williams, email genome@smith.edu."
BASE COUNT     65 a     28 c     33 g     16 t
ORIGIN
Alignment Scores:
Pred. No.:        1.14e+03       Length:        142
```

```
Score:                    28.00         Indels:          0
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:                            Gaps:            0
DB:                       9

US-09-856-070-26 (1-5) x AI130110 (1-142)

Qy    1 GlnAspTyrGluGlu 5
        |||||||||||||||
Db  107 CAAGATTACGAAGAA 121

RESULT 10
BEI70685
LOCUS       BEI70685           148 bp    mRNA    linear    EST 21-JUN-2000
DEFINITION  QV4-HT0539-010500-120-d04 HT0539 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BEI70685
VERSION     BEI70685.1  GI:8633406
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 148)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.F.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20204003
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof Antonio Prudente 109, 4 andar. 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tb-stz-qv4-HT0539-olu
            500-120-a04&ts-2000-03-01&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 6
            High quality sequence stop: 148.
FEATURES             Location/Qualifiers
     source          1..148
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HT0539"
                     /dev_stage="Adult"
                     /note="Organ: head_q--k; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI. A mini library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters patent application
                     No. 796,716; Ludwig Institute for Cancer Research)
                     profiles into the puc 18 vector Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT     57 a     22 c     31 g     38 t
ORIGIN
Alignment Scores:
Pred. No.:        1.21e-03       Length:        148
Score:            28.00          Matches:       5
Percent Similarity:   100.00%    Conservative:  0
Best Local Similarity: 100.00%   Mismatches:    0
Query Match:                     Indels:        0
DB:               10             Gaps:          0
```

US-09-856-070-26 (1-5) x BE170685 (1-148)

Qy   1 GlnAspTyrGluGlu 5
        ||||||||||||||
Db   46 CAGGATTATGAAGAA 50

RESULT 11
LOCUS   BG192942
DEFINITION   RST12057 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG192942
VERSION   BG192942.1 GI:13714619
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 154)
AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
             Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,
             ,E., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
             ,J., Danzig,J. and bucar,M.
TITLE   Creation of genome wide protein expression libraries using random
             activation of gene expression
JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE   21227151
COMMENT   Contact: Scott J. Cain
             Athersys, Inc.
             3201 Carnegie Ave, Cleveland, OH 44115, USA
             Tel: 216 431 9900
             Fax: 216 361 9596
             Email: scain@athersys.com
             High quality sequence stop: 154.
FEATURES   Location/Qualifiers
     source   1..154
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT   62 a   24 c   30 g   38 t
ORIGIN

Alignment Scores:
Pred. No.:   1.28e-03
Score: 28.00
Percent Similarity: 100.00%   Length: 154
Best Local Similarity: 100.00%   Matches: 5
Query Match: 100.00%   Conservative: 0
DB: Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

US-09-856-070-26 (1-5) x BG192932 (1-154)

Qy   1 GlnAspTyrGluGlu 5
        ||||||||||||||
Db   71 CAAGATTACGAAGAG 85

RESULT 12
LOCUS   BM844888
DEFINITION   K RST012C994 S12SNU216 Homo sapiens cDNA clone S12SNU216-93-F08 5'
             mRNA sequence.
ACCESSION   BM844888
VERSION   BM844888.1 GI:19201287
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens

US-09-856-070-26 (1-5) x BE170685 (1-148)

Qy   1 GlnAspTyrGluGlu 5
        ||||||||||||||
Db   46 CAGGATTATGAAGAA 50

LOCUS   BE170685   154 bp   mRNA   linear   EST 21-APR-2001
DEFINITION   RST12057 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE170685
VERSION   BE170685.1 GI:13714619
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 157)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
             Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
             Kim,Y.S.
TITLE   21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
             Genome Research Center
             Korea Research Institute of Bioscience & Biotechnology
             52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
             Tel: +82-42-860-4470
             Fax: +82-42-860-4409
             Email: yongsung@mail.kribb.re.kr
             Plate: 93 row: F column: 08
             High quality sequence stop: 157.
FEATURES   Location/Qualifiers
     source   1..157
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S12SNU216-93-F08"
                     /clone_lib="S12SNU216"
                     /sex="M"
                     /tissue_type="lymph node"
                     /cell_type="epithelial"
                     /cell_line="SNU-216"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
                     Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tobacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT   61 a   30 c   32 g   34 t
ORIGIN

Alignment Scores:
Pred. No.:   1.31e-03
Score: 28.00   Length: 157
Percent Similarity: 100.00%   Matches: 5
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 14   Indels: 0
                                       Gaps: 0

US-09-856-070-26 (1-5) x BM844888 (1-157)

Qy   1 GlnAspTyrGluGlu 5
        ||||||||||||||
Db   39 CAGGATTATGAAGAA 53

RESULT 13
LOCUS   AW867176   159 bp   mRNA   linear   EST 22-MAY-2000
DEFINITION   MR1-SN0045-060400-001-d02 SN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW867176
VERSION   AW867176.1 GI:8201228
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 159)

AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
           Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
           Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
           Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
           ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.T. and
           Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
           sequence tags
JOURNAL   Proc Natl Acad Sci U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
           Laboratory of Cancer Genetics
           Ludwig Institute for Cancer Research
           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           Project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&12-MP1-SN0045-060
           400-001-002&t3-2000-04-06&t4-1)
           Seq primer: puc 18 forward
           High quality sequence start: 4
           High quality sequence stop: 159.
FEATURES   Location/Qualifiers
     source   1..159
                    /organism="Homo sapiens"
                    /db_xref="taxon 9606"
                    /clone_lib="SN0045"
                    /dev_stage "Adult"
                    /note="Organ: stomach_normal; Vector: puc18, Site_1: SmaI;
                    Site_2: SmaI; A mini-library was made by cloning products
                    derived from ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 - Ludwig Institute for Cancer Research)
                    profiles into the puC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
BASE COUNT   59 a   40 c   29 g   31 t
ORIGIN

Alignment Scores:
Pred. No.:   1.34e+03   Length: 159
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: Gaps: 10

US-09-856-070-26 (1-5) x AW867176 (1-159)

Qy   1 GlnAspTyrGluGlu 5
         ||||||||||||||||
Db   42 CAAGACTACGAAGAA 56

RESULT 14
BI013708/c
LOCUS   BI013708   164 bp   mRNA   linear   EST 13-JUN-2001
DEFINITION PM3-ET0207-230101-106-a03 ET0207 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI013708
VERSION   BI013708.1   GI:14417779
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
           Eukaryota. Metazoa. Chordata. Craniata. Vertebrata. Euteleostomi.
           Mammalia; Eutheria. Primates. Catarrhini. Hominidae; Homo.
REFERENCE 1 (bases 1 to 164)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
           Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
           Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
           Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
           ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
           Simpson,A.J.

TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
           sequence tags
JOURNAL   Proc Natl Acad Sci U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
           Laboratory of Cancer Genetics
           Ludwig Institute for Cancer Research
           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           Project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-PM3&12-PM3-ET0207-
           23010106-a03&t3-2001-01-23&t4-1)
           Seq primer: puc 18 forward
           High quality sequence stop: 161.
FEATURES   Location/Qualifiers
     source   1..164
                    /organism="Homo sapiens"
                    /db_xref="taxon 9606"
                    /clone_lib="ET0207"
                    /dev_stage="Adult"
                    /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                    Site_2: SmaI; A mini-library was made by cloning products
                    derived from ORESTES PCR (U.S. Letters Patent application
                    No. 196,716 - Ludwig Institute for Cancer Research)
                    profiles into the puC 18 vector. Reverse transcription of
                    tissue mRNA and cDNA amplification were performed under
                    low stringency conditions."
BASE COUNT   29 a   33 c   57 g   45 t
ORIGIN

Alignment Scores:
Pred. No.:   1.4e+03   Length: 164
Score: 28.00   Matches: 5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 13   Gaps: 0

US-09-856-070-26 (1-5) x BI013708 (1-164)

Qy   1 GlnAspTyrGluGlu 5
         ||||||||||||||||
Db   164 CAAGACTACGAGGAA 150

RESULT 15
AZ227319/c
LOCUS   AZ227319   167 bp   DNA   linear   GSS 14-JUN-2000
DEFINITION RPCI-23-4918 TV RPCI-23 Mus musculus genomic clone RPCI-23-4918,
           DNA sequence.
ACCESSION AZ227319
VERSION   AZ227319.1   GI:8535368
KEYWORDS   GSS.
SOURCE   house mouse.
ORGANISM   Mus musculus
           Eukaryota. Metazoa. Chordata. Craniata. Vertebrata. Euteleostomi.
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 167)
AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinro
           ,B., Levins,M., Mcgann,S., Tseqaye,G., Geer,K., Krol,M., de Jrug,P.
           and Fraser,C.M.
TITLE   Mouse BAC End Sequences from library RPCI-23
JOURNAL   Unpublished (1999)
COMMENT   Other_GSSs: RPCI-23-4918.TJ
           Contact: Shaying Zhao
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr, Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208

```
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Reseach Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_ends_intro.html
Seq primer: T7
Plate: 49  row: I  column: 8
Class: BAC ends.

FEATURES             Location/Qualifiers
     source          1..167
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-491B"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="organ: Kidney/Brain, Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI  Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies)."
BASE COUNT      44 a      27 c      25 g      71 t
ORIGIN

Alignment Scores:
Pred. No.:              1.4e+03       Length:        167
Score:                  28.00         Matches:       5
Percent Similarity:     100.00%       Conservative:  0
Best local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     17            Gaps:          0

US 09-856-070-26 (1-5) x AZ227319 (1-167)

Qy    1 GlnAspTyrGluGlu 5
        |||||||||||||||
Db  159 CAGGACTATGAAGAA 145

Search completed: January 16, 2003, 21:37:14
Job time : 664.571 secs
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